



## SEQUENCE LISTING

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<120> Production of Oligosaccharides in Transgenic Plants

<130> ARNO-1-15313

<140> US 09/543,861  
<141> 2000-03-24

<150> US 09/019,385  
<151> 1998-02-05

<150> US 08/479,470  
<151> 1995-06-07

<150> NL 1000064  
<151> 1995-04-05

<150> NL 9401140  
<151> 1994-08-07

<160> 12

<170> PatentIn version 3.0

<210> 1  
<211> 2094  
<212> DNA  
<213> Barley

<220>

<221> CDS

<222> (46)..(1923)

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57

Met Gly Ser His

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gac aag cca ccg cta ccg tac gcc tac aag ccg ctg ccc tcg gac gcc

105  
 Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu Pro Ser Asp Ala  
 5 10 15 20

gcc gac ggt aag cgg acc ggc tgc atg agg tgg tcc gcg tgt gcc acc  
 153  
 Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser Ala Cys Ala Thr  
 25 30 35

gtg ctg acg gcc tcg gcc atg gcg gtg gtg gtg gtc ggc gcc acg ctc  
 201  
 Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val Gly Ala Thr Leu  
 40 45 50

ctg gcg gga ttg agg atg gag cag gcc gtc gac gag gag gcg gcg gcg  
 249  
 Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu Glu Ala Ala Ala  
 55 60 65

ggc ggg ttc ccg tgg agc aac gag atg ctg cag tgg cag cgc agc ggt  
 297  
 Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp Gln Arg Ser Gly  
 70 75 80

tac cat ttc cag acg gcc aag aac tac atg agc gat ccc aac ggc ctg  
 345  
 Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu  
 85 90 95 100

atg tat tac cgt gga tgg tac cac atg ttc tac cag tac aac ccg gtg  
 393  
 Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Prc Val  
 105 110 115

ggc acc gac tgg gac gac ggc atg gag tgg ggc cac gcc gtg tcc cgg  
 441

Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg

120

125

130

aac ctt gtc caa tgg cgc acc ctc cct atc gcs atg gtg gcc gac cag  
 489

Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met Val Ala Asp Gln

135

140

145

tgg tac gac atc ctc gga gtc ctc tgg ggc tcs atg acg gtg cta ccc  
 537

Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met Thr Val Leu Pro

150

155

160

aac ggg acg gtc atc atg atc tac acg ggc gcc acc aac gcc tcc gcs  
 585

Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr Asn Ala Ser Ala

165

170

175

180

gtg gag gtc cag tgc atc gcc acc ccg gcc gac ccc aac gac ccc ctc  
 633

Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro Asn Asp Pro Leu

185

190

195

ctc cgc cgg tgg acc aag cac ccc gcc aac ccc gtc atc tgg tgg ccg  
 681

Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val Ile Trp Ser Pro

200

205

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ccg ggg gtc ggc acc aag gat ttc cga gac ccg atg acc gcc tgg tac  
 729

Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met Thr Ala Trp Tyr

215

220

225

gac gag tcc gac gag aca tgg cgc acc ctc ctc ggg tcc aag gac gac  
 777

Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly Ser Lys Asp Asp

230

235

240

cac gac ggc cac cac gac ggc atc gcc atg atg tac aag acc aag gac  
 825

His Asp Gly His His Asp Gly Ile Ala Met Met Tyr Lys Thr Lys Asp

245

250

255

260

tcc ctc aac tac gag ctc atc ccg ggc atc ttg cac cgg gtg gtg cgc  
 873

Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His Arg Val Val Arg

265

270

275

acc ggc gag tgg gag tgc atc gac ttc tac ccc gtc ggc cgg aga agc  
 921

Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg Arg Ser

280

285

290

agc gac aac tcg tcg gag atg ctg cac gtg ttg aag gcg agc atg gac  
 969

Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys Ala Ser Met Asp

295

300

305

gac gaa cgg cac gac tac tac tcg ctg ggc acg tac gac tcg gcg gcc  
 1017

Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr Asp Ser Ala Ala

310

315

320

aac acg tgg acg ccc atc gac ccg gag ctc gac ttg ggg atc ggg ctg  
 1065

Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu Gly Ile Gly Leu

325

330

335

340

aga tac gac tgg gga aag ttt tat gcg tcc acc tcc ttc tat gat csg  
 1113

Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe Tyr Asp Pro

345

350

355

gcc aag aac cgg cgc gtg ctc atg ggg tac gtc ggc gag gtc gac tcc  
 1161

Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly Glu Val Asp Ser

360

365

370

aag cgg gct gat gtc gtc aag gga tgg gct tcc att cag tca gtt cct  
 1209

Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile Gln Ser Val Pro

375

380

385

agg acg gtg gct ctg gat gag aag acc cgg acg aac ctc ctg ctc tgg  
 1257

Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn Leu Leu Leu Trp

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ccc gtt gag gag atc gag acc ctc cgc ctc aat gcc acg gaa ctg acc  
 1305

Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala Thr Glu Leu Thr

405

410

415

420

gac gtt acc att aac act ggc tcc gtc atc cat atc ccg ctc cgc caa  
 1353

Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile Pro Leu Arg Gln

425

430

435

ggc act cac gct cga cat gcg gag gcc tct ttc cac ctt gat gct tcc  
 1401

Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His Leu Asp Ala Ser

440

445

450

gcc gtg gct gcc ctc aac gag gag gat gtg ggc tac aac tgc agt agc  
 1449

Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr Asn Cys Ser Ser

455

460

465

agc ggc ggc gct gtt aac cgc ggc gcg cta ggc ccc ttc ggc ctc ctc  
 1497

Ser Gly Ala Val Asn Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu

470

475

480

gtc ctc gcc ggc ggt gac cgc cgt ggc gag caa aac gcg gtc tac ttc  
 1545

Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr Ala Val Tyr Phe

485

490

495

500

tac gtg tct agg ggc ctt gac gga ggc ctc cac acc aac ttc tgc caa  
 1593

Tyr Val Ser Arg Gly Leu Asp Gly Leu His Thr Ser Phe Cys Gln

505

510

515

gat gag ctg aga tcg tca cga gcc aag gat gtg acc aac cgt gtc atc  
 1641

Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr Lys Arg Val Ile

520

525

530

ggg aac acg gtg ccg gtg ctc gac ggt gag gct ttg tca atg agg gtg  
 1689

Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu Ser Met Arg Val

535

540

545

ctc gtg gat cac tcc atc gtg cag ggc ttc gac atg ggc ggg agg acc  
 1737

Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met Gly Gly Arg Thr

550

555

560

acg atg acc tcg cgg gtg tac ccg atg gag tcg tat cag gag gca aga  
 1735  
 Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr Gln Glu Ala Arg

565

570

575

580

gtc tac ttg ttc aac aac gcc acc ggt gcc agc gtg acg gcg gaa agg  
 1833  
 Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val Thr Ala Glu Arg

585

590

595

ctg gtc gtg cac gag atg gac tcg gca cac aac cag ctc tcc aat gag  
 1881  
 Leu Val Val His Glu Met Asp Ser Ala His Asn Gln Leu Ser Asn Glu

600

605

610

gac gat ggc atg tat ctt cat caa gtt ctt gaa tct cgt cat  
 1923  
 Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser Arg His

615

620

625

taataagcta cattggatca aagaagatca ccagggagg gcaattcata cataaatcga  
 1983

atcattctgc acaacctcgc ttgcagcatg cattgaaaca tctgtatttg gatcatcttc  
 2043

ttcatttatg tcatagtcaa ctatattact ttgtaaaaaa aaaaaaaaaa a  
 2094

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 <212> PRT  
 <213> Barley

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Met Gly Ser His Gly Lys Pro Pro Leu Pro Tyr Ala Tyr Lys Pro Leu  
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Pro Ser Asp Ala Ala Asp Gly Lys Arg Thr Gly Cys Met Arg Trp Ser  
20 25 30

Ala Cys Ala Thr Val Leu Thr Ala Ser Ala Met Ala Val Val Val Val  
35 40 45

Gly Ala Thr Leu Leu Ala Gly Leu Arg Met Glu Gln Ala Val Asp Glu  
50 55 60

Glu Ala Ala Ala Gly Gly Phe Pro Trp Ser Asn Glu Met Leu Gln Trp  
65 70 75 80

Gln Arg Ser Gly Tyr His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp  
85 90 95

Pro Asn Gly Leu Met Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln  
100 105 110

Tyr Asn Pro Val Gly Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His  
115 120 125

Ala Val Ser Arg Asn Leu Val Gln Trp Arg Thr Leu Pro Ile Ala Met  
130 135 140

Val Ala Asp Gln Trp Tyr Asp Ile Leu Gly Val Leu Ser Gly Ser Met  
145 150 155 160

Thr Val Leu Pro Asn Gly Thr Val Ile Met Ile Tyr Thr Gly Ala Thr  
165 170 175

Asn Ala Ser Ala Val Glu Val Gln Cys Ile Ala Thr Pro Ala Asp Pro  
180 185 190

Asn Asp Pro Leu Leu Arg Arg Trp Thr Lys His Pro Ala Asn Pro Val  
195 200 205

Ile Trp Ser Pro Pro Gly Val Gly Thr Lys Asp Phe Arg Asp Pro Met  
210 215 220

Thr Ala Trp Tyr Asp Glu Ser Asp Glu Thr Trp Arg Thr Leu Leu Gly  
225 230 235 240

Ser Lys Asp Asp His Asp Gly His His Asp Gly Ile Ala Met Met Tyr  
245 250 255

Lys Thr Lys Asp Phe Leu Asn Tyr Glu Leu Ile Pro Gly Ile Leu His  
260 265 270

Arg Val Val Arg Thr Gly Glu Trp Glu Cys Ile Asp Phe Tyr Pro Val  
275 280 285

Gly Arg Arg Ser Ser Asp Asn Ser Ser Glu Met Leu His Val Leu Lys  
290 295 300

Ala Ser Met Asp Asp Glu Arg His Asp Tyr Tyr Ser Leu Gly Thr Tyr  
305 310 315 320

Asp Ser Ala Ala Asn Thr Trp Thr Pro Ile Asp Pro Glu Leu Asp Leu  
325 330 335

Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser  
340 345 350

Phe Tyr Asp Pro Ala Lys Asn Arg Arg Val Leu Met Gly Tyr Val Gly  
355 360 365

Glu Val Asp Ser Lys Arg Ala Asp Val Val Lys Gly Trp Ala Ser Ile  
370 375 380

Gln Ser Val Pro Arg Thr Val Ala Leu Asp Glu Lys Thr Arg Thr Asn  
385 390 395 400

Leu Leu Leu Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Leu Asn Ala  
405 410 415

Thr Glu Leu Thr Asp Val Thr Ile Asn Thr Gly Ser Val Ile His Ile  
420 425 430

Pro Leu Arg Gln Gly Thr His Ala Arg His Ala Glu Ala Ser Phe His  
435 440 445

Leu Asp Ala Ser Ala Val Ala Ala Leu Asn Glu Ala Asp Val Gly Tyr  
450 455 460

Asn Cys Ser Ser Ser Gly Gly Ala Val Asn Arg Gly Ala Leu Gly Pro  
465 470 475 480

Phe Gly Leu Leu Val Leu Ala Ala Gly Asp Arg Arg Gly Glu Gln Thr  
485 490 495

Ala Val Tyr Phe Tyr Val Ser Arg Gly Leu Asp Gly Gly Leu His Thr  
500 505 510

Ser Phe Cys Gln Asp Glu Leu Arg Ser Ser Arg Ala Lys Asp Val Thr  
515 520 525

Lys Arg Val Ile Gly Ser Thr Val Pro Val Leu Asp Gly Glu Ala Leu  
530 535 540

Ser Met Arg Val Leu Val Asp His Ser Ile Val Gln Gly Phe Asp Met  
545 550 555 560

Gly Gly Arg Thr Thr Met Thr Ser Arg Val Tyr Pro Met Glu Ser Tyr  
565 570 575

Gln Glu Ala Arg Val Tyr Leu Phe Asn Asn Ala Thr Gly Ala Ser Val  
580 585 590

Thr Ala Glu Arg Leu Val Val His Glu Met Asp Ser Ala His Asn Gln  
595 600 605

Leu Ser Asn Glu Asp Asp Gly Met Tyr Leu His Gln Val Leu Glu Ser  
610 615 620

Arg His  
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<210> 4  
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cgcctgcagg taccacatgt tytaycarta yaaycc  
36

<210> 5  
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<212> DNA  
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ccacgtcttag agctctcrtc rtaccavgcs gtcatt  
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<213> Peptide

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His Phe Gln Thr Ala Lys Asn Tyr Met Ser Asp Pro Asn Gly Leu Met  
1 5 10 15

Tyr Tyr Arg Gly Trp Tyr His Met Phe Tyr Gln Tyr Asn Pro Val Gly  
20 25 30

Thr Asp Trp Asp Asp Gly Met Glu Trp Gly His Ala Val Ser Arg  
35 40 45

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<212> PRT  
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Trp Glu Cys Ile Asp Phe Tyr Pro Val Gly Arg  
1 5 10

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<212> PRT  
<213> Peptide

<400> 8

Ser Gly Ser Met Thr Val Leu Pro  
1 5

<210> 9  
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<212> PRT  
<213> Peptide

<400> 9

Phe Arg Asp Pro Met Thr Ala Trp Tyr Asp  
1 5 10

<210> 10  
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<212> PRT

<213> Peptide

<400> 10

Asp Trp Gly Lys Phe Tyr Ala Ser Thr Ser Phe  
1 5 10

<210> 11

<211> 13

<212> FRT

<213> Peptide

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<221> misc\_feature

<222> (1)..(13)

<223> Xaa is the nucleotide equivalent of any set containing "n"

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Glu Gln Trp Glu Gly Xaa Phe Met Gln Gln Tyr Xaa Xaa  
1 5 10

<210> 12

<211> 15

<212> FRT

<213> Peptide

<220>

<221> misc\_feature

<222> (1)..(15)

<223> Xaa in position 11 is either phenylalanine or leucine

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Ala Val Pro Val Xaa Leu Xaa Xaa Pro Leu Xaa Ile Xaa Trp Val  
1 5 10 15